AMENDMENT

In the Specification:

Please amend the paragraph beginning at page 26, line 20, as follows:

The sequences of the oligonucleotides used in the following examples are set forth in Table 1:

Table 1

Oligo name	Oligo 70mer sequence (L = NH2)	Genbank accession	Gene name	SEQ ID NO:
h-136	LTTGAGCAGTGGGCTCACTCTGAAGA CCTGCAGTCCCTCCTGCTTAGGGTCG CTAATGCTGTTTCGGTGAA	U56390	Caspase 9	1
h-252	LCCGCGCCGACAAACAGAACCTGGA GGCCATTCTGCACAGCCTGCCCGAGA ACTGTGCCAGCTGGCAGTGA	AF041835	Laminin γ3 precursor; LAMC3	2
h-501-b	LGCTCCCAGAATTTCAGCTTCAGCTT AACTGACAGATGTTAAAGCTTTCTGG TTAGATTGTTTTCACTTGC	K00558	Alpha-tubulin	3
h-503-b	LCCACCTGTCCCTCCTGGGCTGCTGG	U14971	Ribosomal	
	ATTGTCTCGTTTTCCTGCCAAATAAA CAGGATCAGCGCTTTAAAA		protein S9	4
	50mer complement with biotin at 5' end (X = biotin)			
h-136r50	XTTCACCGAAACAGCATTAGCGACCC TAAGCAGGAGGGACTGCAGGTCTTC			5
h-252r50	XTCACTGCCAGCTGGCACAGTTCTCG GGCAGGCTGTGCAGAATGGCCTCCA			6
h-501-br50	XCCAAGTGAAAACAATCTAACCAGA AAGCTTTAACATCTGTCAGTTAAGCT			7
h-503-br50	XTTTTAAAGCGCTGATCCTGTTTATTT GGCAGGAAAACGAGACAATCCAGC			8

	Complement oligo with generic tag			
c186-h-136	**G GCG TGG CGG GGA AAG CAT** TTCACCGAAACAGCATTAGCGACCCT AAGCAGGAGGGACTGCAGGTCTTC			9
clambda-h-136	**GGG CGG CGA CCT T** TTCACCGAAACAGCATTAGCGACCCT AAGCAGGAGGGACTGCAGGTCTTC			10
clambda-h-252	**GGG CGG CGA CCT T** TCACTGCCAGCTGGCACAGTTCTCGG GCAGGCTGTGCAGAATGGCCTCCA			11
c186-h-252	**G GCG TGG CGG GGA AAG CAT** TCACTGCCAGCTGGCACAGTTCTCGG GCAGGCTGTGCAGAATGGCCTCCA			12
	Oligos for attachment to SCNCs			
B-lambda CATCH	5' -Biotin- CTG GAA CAA CAC TCA CAA GGT CGC CGC CC -3'			13
B-186 CATCH	5' -Biotin- CTG GAA CAA CAC TCA CAA TGC TTT CCC CGC CAC GCC -3'			14

Please amend the paragraph beginning at page 30, line 16, as follows:

This experiment demonstrates that detection of polynucleotides on an array using probe polynucleotides comprising a tag sequence produces equivalent results to probe polynucleotides lacking a tag. A reverse transcription primer (RT186) was designed. This sequence of this primer is 5'-GGCGTGGCGGGGAAAGCATTTTTTT TTTTTTTTTTTTTTVN-3' (SEQ ID NO:15). The 5' extension of the primer is identical to one of the strands of the bacteriophage 186 cos site. Such sites serve the purpose of forming hybrids at physiological temperatures, driving circularization of phage genomes in their host cells. The inclusion of a 5' extension readily able to hybridize to its complement at modest temperatures (25-37 C) is intended to allow a two hybridization approach to quantitating mRNA transcripts with microarrays. In the first step, cDNAs synthesized from sample RNAs using the extended primer are hybridized in a high temperature, stringent hybridization to a microarray. After the first hybridization, non-hybridized strands are removed and then a second, low-temperature hybridization is carried out with semiconductor nanocrystals derivatized with oligonucleotides that are the complement of the 5' extension of the hybridized strands. One requirement for this approach to work is that the 5' extension not cause spurious hybridization to the immobilized cDNAs during the first, stringent hybridization.